REMARKS

Entry of the foregoing prior to the initial office action on the merits is respectfully requested. Pursuant to 37 C.F.R. § 1.121, attached as Appendix A is a version with markings to show changes made to the specification and claims.

Respectfully submitted,

Date: March 22, 2002

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APPENDIX A

Version With Markings to Show Changes Made

In reference to the amendments made herein to the specification and claims 5, 9, 11, 13, and 15, additions appear as underlined text, while deletions appear as bracketed text, as indicated below:

In the Specification:

Page 3, line 32 to page 4, line 1 should be changed to read as follows:

The present inventors, after conducting extensive studies to solve the above-mentioned problems, thought that the electrophoresis using a small-sized gel, which is generally used in electrophoresis of proteins, could be appropriately used to perform electrophoresis of a large number of nucleic acid[s] samples efficiently and detect nucleic acid[s] bands of interest.

Page 16, lines 9 to 11 should be changed to read as follows:

In this application, although combination of n bands enables identification of up to 2n breeds/lines theoretically (where n is an integer), it may be slightly less than that practically.

Page 21, line 31 to page 22, line 14 should be changed to read as follows:

To achieve almost one-to-one correspondence between the AFLP bands and the library clones, the genomic library for the entire genome, which generally has several genome equivalents or more, is divided into several sublibraries of approximately 1 genome equivalent each. Each component clone of the sublibraries is uniquely identified by coordinate of row, column, and plate numbers of the microplate. Therefore, using row, column, and plate numbers as coordinate axes, small amounts of DNAs are collected from groups of clones with a common axis coordinates, and mixed to provide coordinate samples representing positions on each axis. By performing genome scanning of the present invention using these coordinate samples as templates and comparing AFLP patterns with control lanes, which are prepared by using whole genome DNA as templates, placed on both sides of the coordinate lanes, clones corresponding to specific bands from the genomic DNA templates are readily detected from the sublibrary. When there are 2 to n corresponding clones in the sub-group (where n is an integer), $2^3 = 8$ to n^3 clones correspond to the bands. In this case, by

removing these 8 clones and performing second electrophoresis of the genome scanning method, the truly corresponding 2 clones are identified. Specific procedures to prepare coordination samples of a sublibrary are shown in Example 5.

In the Claims:

5. The method according to [any one of claims 1, 2, or 4] claim 1, wherein the method is performed in order to detect a polymorphism of genomic DNAs among test individuals.

9. A method for preparing DNA fragments comprising a polymorphism, said method comprising a step of isolating, from gels, DNA fragments comprising a polymorphism detected by the method according to [any one of claims 5 through 8] claim 5.

11. The method according to [any one of claims 1 through 8] claim 1, wherein the method is performed in order to carry out genetic analysis.

13. The method according to [any one of claims 1 through 8] claim 1, which is performed to construct a genetic map of an organism.

15. A method for selecting, from a genomic DNA library, a clone corresponding to a particular nucleic acid band on a gel detected by the method according to [any one of claims 1 through 8] claim 1, said method comprising the following steps:

a) dividing a genomic DNA library of a particular organism into plural sublibraries each of which has a size of 1 or less genome of the organism;

b) assigning, to all clones included in each of the sublibraries, a row number, a column number, and a plate number of the sublibrary, wherein the row, column, and plate are referred to as X coordinate, Y coordinate, and Z coordinate, respectively;

c) detecting a band by collecting clones representing a particular row of all plates (X-coordinate clone group), clones representing a particular column of all plates (Y-coordinate clone group), and all clones on a particular plate of one sublibrary (Z-coordinate clone group); by extracting DNAs from each of the collected clone groups to obtain coordinate samples; by preparing a genomic DNA from the organism as a control; and by

electrophoresing the coordinate samples and the control in a line using the method according to [any one of claims 1 through 4] claim 1;

d) determining a clone in each of the X-coordinate clone group, the Y-coordinate clone group, and the Z-coordinate clone group, said clone corresponding to a band with the same mobility on the gel as that of the nucleic acid of interest in the control; and

e) selecting, from the sublibrary, a clone corresponding to the determined three-dimensional coordinate.